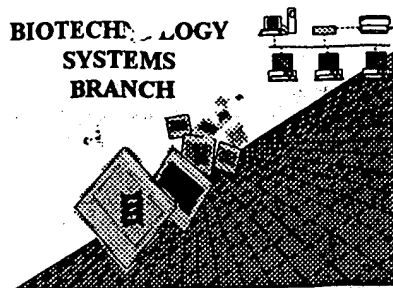


BEST AVAILABLE COPY

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/845,612
Source: OIR
Date Processed by STIC: 5/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, -703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09845,612

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
 <400> sequence id number
 000

- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.

- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/845,612

DATE: 05/11/2001

TIME: 14:29:11

Input Set : A:\ES.txt

Output Set: N:\CRF3\05112001\I845612.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: YU, HONGTAO
 4 TANG, ZHANYUN
 5 LUO, XUELIAN
 6 RIZO-REY, JOSE
 8 <120> TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOTIC
 CHECK
 9 POINT PROTEIN MAD2
 11 <130> FILE REFERENCE: UTSD:0795
 13 <140> CURRENT APPLICATION NUMBER: US/09/845,612
 14 <141> CURRENT FILING DATE: 2001-04-30
 15 <160> NUMBER OF SEQ ID: 20
 17 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

332 <210> SEQ ID NO: 20
 333 <211> LENGTH: 11
 334 <212> TYPE: PRT
 335 <213> ORGANISM: HIV-TAT PROTEIN
 337 <400> SEQUENCE: 20
 - 339 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg
 340 1 5 10
 342 25025713.1
 E--> 343 4
 E--> 344 Express Mail No. EH244916502US

delete at end of file

PI ase Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

see next page for more errors

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<210> 1

<211> 8

<212> PRT

<213> Artificial

See item 11 on End Summary Sheet

<220>

<223> Synthetic Peptide

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/845,612

DATE: 05/11/2001

TIME: 14:29:13

Input Set : A:\ES.txt

Output Set: N:\CRF3\05112001\I845612.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:22 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:343 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
L:344 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:344 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:344 M:252 E: No. of Seq. differs, <211>LENGTH:Input:11 Found:15 SEQ:20